

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 17, 2003, 14:04:54 ; Search time 1 Seconds

(without alignments)
6.964 Million cell updates/sec

Title: us-09-944-896-49

Perfect score: 1876

Sequence: 1 cctcttgcacacagccca.....tcagctgaataaaaaaa 1876

Scoring table: IDENTITY-NIC
Gapop 10.0 , Gapext 0.5

Searched: 1 seqs, 1856 residues
Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database: seq264-1.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	1764.5	94.1	1856	1 us-09-790-264-1
2	25.8	1.4	1856	1 us-09-790-264-1

ALIGNMENTS

RESULT 1
us-09-790-264-1

Query Match 94.1%; Score 1764.5; DB 1; Length 1856;
Best Local Similarity 98.0%; Pred. No. 0;
Matches 1794; Conservative 0; Mismatches 10; Indels 27; Gaps 1;

QY	46	GCCTCATCCAGCCCTGGAAGAACAGCCGGGTGGCTGAGCCAGGCTGTGACGAGACCTG	105
DB	18	GCCTCATCCAGCCCTGGAAGAACAGCCGGGTGGCTGAGCCAGGCTGTGACGAGACCTG	77
QY	106	ACGGGCCCAACAGACCCATGCTGATCCAGAGACTCCCTGGCCGGGGGCACTCTCCG	165
DB	78	ACGGGCCCAACAGACCCATGCTGATCCAGAGACTCCCTGGCCGGGGGCACTCTCCG	137
QY	166	CTGTGCTCTGCGCCCTCTTGGACCACTGGGAGAGGTGTGGCCACCCAGCTGAGG	225
DB	138	CTGTGCTCTGCGCCCTCTTGGACCACTGGGAGAGGTGTGGCCACCCAGCTGAGG	197
QY	226	AGCAGGCTCGAGAGGCGCGGAGCCCTGAACAGAGAGTTTCTGCTCTCCCTCC	285
DB	198	AGCAGGCTCGAGAGGCGCGGAGCCCTGAACAGAGAGTTTCTGCTCTCCCTCC	257
QY	286	ACAACCGCTGCGCAGCTGGCTCAGGCCCCCTGGGGCTGACATGCGAGGCTGAC	345
DB	258	ACAACCGCTGCGCAGCTGGCTCAGGCCCCCTGGGGCTGACATGCGAGGCTGAC	317

Sequence Alignment

QY	346	GTGACAGCCCTGGCCCACTGCTCAAGCCAGGGCAGCCCTGTGTGAATCCCAACCCCGA	405
DB	318	GTGACAGCCCTGGCCCACTGCTCAAGCCAGGGCAGCCCTGTGTGAATCCCAACCCCGA	377
QY	406	GCCCTGATCCGCGCTGTGGCGCAGCCCTGGAAGTGGGCTGGAACTCAGCTGTGCGG	465
DB	378	GCCCTGATCCGCGCTGTGGCGCAGCCCTGGAAGTGGGCTGGAACTCAGCTGTGCGG	437
QY	466	CGGGCTTGGCTCTTGTGAAGTGTCAAGCTTATGTTTGGAGAGGGGAGCGGTACA	525
DB	438	CGGGCTTGGCTCTTGTGAAGTGTCAAGCTTATGTTTGGAGAGGGGAGCGGTACA	497
QY	526	GCCACGCGCAGAGAGTGTGCTCGAAGCCCACTGCAACCCATCAGCAGCTGTGT	585
DB	498	GCCACGCGCAGAGAGTGTGCTCGAAGCCCACTGCAACCCATCAGCAGCTGTGT	557
QY	586	GGGCCACTCAAGCCAGCTGGGCTGTGGCGGACCTGTGCTGCAAGGCGCAGACGA	645
DB	558	GGGCCACTCAAGCCAGCTGGGCTGTGGCGGACCTGTGCTGCAAGGCGCAGACGA	617
QY	646	TAGAAGCTTGTCTGTGCTACTCCCCGAGAGCACTGGAGGTCAACGGGAGACAA	705
DB	618	TAGAAGCTTGTCTGTGCTACTCCCCGAGAGCACTGGAGGTCAACGGGAGACAA	677
QY	706	TCATCCCTTATAGAAGAGGTGCTGTGCTGTGCTGCAAGCCAGTGTCTCAGGCTGT	765
DB	678	TCATCCCTTATAGAAGAGGTGCTGTGCTGTGCTGCAAGCCAGTGTCTCAGGCTGT	737
QY	766	TCAAGCTTGGAGCATCAGAGGGGCTGTGTGAGGTCCCAAGATCCCTTGTGCGATGA	825
DB	738	TCAAGCTTGGAGCATCAGAGGGGCTGTGTGAGGTCCCAAGATCCCTTGTGCGATGA	797
QY	826	GCTGCGAAGCAATGAGAGTCTCAACATCAGACCTGCCACTGTCCCTGCTGCT	885
DB	798	GCTGCGAAGCAATGAGAGTCTCAACATCAGACCTGCCACTGTCCCTGCTGCT	857
QY	886	ACAGGGCAGATATCTGCCAAGTGAAGTGCAGGCTCAGTGTGACGGCGGGTCCGGG	945
DB	858	ACAGGGCAGATATCTGCCAAGTGAAGTGCAGGCTCAGTGTGACGGCGGGTCCGGG	917
QY	946	AGGAGAGTGTCTGCTGTGATCATCGGCTACGGGGGAGCCAGTGTGACCAAGG	1005
DB	918	AGGAGAGTGTCTGCTGTGATCATCGGCTACGGGGGAGCCAGTGTGACCAAGG	977
QY	1006	TGCATTTCCCTTCCACACCGTGACCTGAGAGATCGAGGAGCTTCTCATGTGTCTT	1065
DB	978	TGCATTTCCCTTCCACACCGTGAGCTGAGAGATCGAGGAGCTTCTCATGTGTCTT	1037
QY	1066	CAGAGCAGACACCTATTACAGAGCCAGATGAATGCAAGGAAAGCGGGGCTGGG	1125
DB	1038	CAGAGCAGACACCTATTACAGAGCCAGATGAATGCAAGGAAAGCGGGGCTGGG	1097
QY	1126	CCGAGATCAAGACCCAGAAAGTGCAGACATCTGCTTATCTGTGGCCGCTGAGGA	1185
DB	1098	CCGAGATCAAGACCCAGAAAGTGCAGACATCTGCTTATCTGTGGCCGCTGAGGA	1157
QY	1186	CCACCAAGAGGTGACATGAGTGTGAGACCAAGAACTTGTGATGCGGCTCACT	1245
DB	1158	CCACCAAGAGGTGATGAGTGTGAGACCAAGAACTTGTGATGCGGCTCACT	1217
QY	1246	ACAAGACCGCAAGGACTCTTCCGTGGGCGCAGAGGGAGCACAGGCTTCAACAGT	1305
DB	1218	ACAAGACCGCAAGGACTCTTCCGTGGGCGCAGAGGGAGCACAGGCTTCAACAGT	1277
QY	1306	TTGCTTTGGGAGCGCTGCAACCAAGGGCTGTGTGTGCTGATGCTCCATGGGCTTG	1365
DB	1278	TTGCTTTGGGAGCGCTGCAACCAAGGGCTGTGTGTGCTGATGCTCCATGGGCTTG	1310
QY	1366	GCAACTGCTGAGGCTGACAGGCTTCACTGCTTCAACTGGAGGAGCCAGGCTGAAAA	1425
DB	1311	GCAACTGCTGAGGCTGACAGGCTTCACTGCTTCAACTGGAGGAGCCAGGCTGAAAA	1370

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OY 1426 CCCGAAACCGTTACATCTGCCAGTTTGGCCAGAGACATCTCCCGGTGGGCCCGAGGGT 1485
    |||||||
DB 1371 CCCGAAACCGTTACATCTGCCAGTTTGGCCAGAGACATCTCCCGGTGGGCCCGAGGGT 1430
    |||||||
OY 1486 CCTGAGGCCCTGACACATGGGCTCCCTGCGCTGCGCTGGAGACCGGCTCTGCTTACCTG 1545
    |||||||
DB 1431 CCTGAGGCCCTGACACATGGGCTCCCTGCGCTGCGCTGGAGACCGGCTCTGCTTACCTG 1490
    |||||||
OY 1546 TCTGCCACCTGTCTGGAACAAGGCCAGGTTAAGACCATGCTCATGTCCAAAGAGG 1605
    |||||||
DB 1491 TCGGCCACCTGTCTGGAACAAGGCCAGGTTAAGACCATGCTCATGTCCAAAGAGG 1550
    |||||||
OY 1606 TCTCAGACCTTGCCATGCGCAGAGAGTGGGCGAGAGAGAGGCGAGGCGCAGTGAAGGC 1665
    |||||||
DB 1551 TCTCAGACCTTGCCATGCGCAGAGAGTGGGCGAGAGAGAGGCGAGGCGCAGTGAAGGC 1610
    |||||||
OY 1666 CAGGAGGTGAGTGTAGAAAGCTGGGGCCCTTGCCCTGCTTTGATTGGGAAGATGGG 1725
    |||||||
DB 1611 CAGGAGGTGAGTGTAGAAAGCTGGGGCCCTTGCCCTGCTTTGATTGGGAAGATGGG 1670
    |||||||
OY 1726 CTTCAATTAGATGGCGAAGAGAGACACCGCCAGTGTCCAAAAAGCTGCTCTTCC 1785
    |||||||
DB 1671 CTTCAATTAGATGGCGAAGAGAGACACCGCCAGTGTCCAAAAAGCTGCTCTTCC 1730
    |||||||
OY 1786 ACCTGGCCCGACCGCTGTGGGGCAGCGAGCTTCCCTGGCATGAACCCACGGGGTAT 1845
    |||||||
DB 1731 ACCTGGCCCGACCGCTGTGGGGCAGCGAGCTTCCCTGGCATGAACCCACGGGGTAT 1790
    |||||||
OY 1846 TAAATTATGATCAGCTGAAAAA 1876
    |||||||
DB 1791 TAAATTATGATCAGCTGAAAAA 1821
    |||||||
```

RESULT 2
us-09-790-264-1/c

Query Match 1.4%: Score 25.8; DB 1; Length 1856;
Best Local Similarity 67.9%; Pred. No. 0;
Matches 36; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

```
OY 1124 GGCCCAATCAAGAGCCAGAAAGTCAGAGACATCTGCGCTTCTATCTGGGCC 1176
    |||||||
DB 1148 GGCCCAATCAAGAGCCAGAGATGTCCTGCACTTCTGCGCTTCTGATCTGGGCC 1096
    |||||||
```

Search completed: September 17, 2003, 14:04:57
Job time : 2 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 17, 2003, 14:00:33 ; Search time 0.001 seconds
(without alignments)
202.930 Million cell updates/sec

Title: us-09-944-896-50

Perfect score: 2529

Sequence: 1 MLHPETSPGRGHLAVLAL.....RNRYICQFAQEHISRMPGS 455

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1 seqs, 446 residues

Total number of hits satisfying chosen parameters: 1

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : seq264-2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Score	Match length	ID	Description
1	2447.5	96.8	446	1 us-09-790-264-2

ALIGNMENTS

RESULT 1
us-09-790-264-2

Query Match 96.8% ; Score 2447.5 ; DB 1 ; Length 446 ;
Best Local Similarity 97.1% ; Pred. No. 0 ;

Matches 442 ; Conservative 1 ; Mismatches 3 ; Indels 9 ; Gaps 1 ;

QY	1	MLHPETSPGRGHLAVLALIGTWAEEVWPPLOEQAPMAGALNKRKESFLLSLNHRIRS	60
DB	1	MLHPETSPGRGHLAVLALIGTWAEEVWPPLOEQAPMAGALNKRKESFLLSLNHRIRS	60
QY	61	WVOPPADMRRLDMSDSLQAOARALCGIPTPSLASGLWRTLOVGMNOLLPGIASF	120
DB	61	WVOPPADMRRLDMSDSLQAOARALCGIPTPSLASGLWRTLOVGMNOLLPGIASF	120
QY	121	VEVYSLMEFAGGORSYSHAGECARNATCTHYTOLWATSSQLCGRHLCSAGQATAEAFVC	180
DB	121	VEVYSLMEFAGGORSYSHAGECARNATCTHYTOLWATSSQLCGRHLCSAGQATAEAFVC	180
QY	181	AYSPGNGMEVNGKTIIPYKKGAMCSLCTASVSGCFKAMDHAGGLCEVPRNRCMSCQNHG	240
DB	181	AYSPGNGMEVNGKTIIPYKKGAMCSLCTASVSGCFKAMDHAGGLCEVPRNRCMSCQNHG	240
QY	241	RLNISTCHCHCPPEYTGRTYQVRCSLQCVHGRFREECSCYCDIGYGAQCATKYHFFPH	300
DB	241	RLNISTCHCHCPPEYTGRTYQVRCSLQCVHGRFREECSCYCDIGYGAQCATKYHFFPH	300

QY	301	TCDLRIDGCFMYSSSEADTYRRAMKQCRKGVLAQIKSOKVODILAEYIGRLTETNEVT	360
DB	301	TCDLRIDGCFMYSSSEADTYRRAMKQCRKGVLAQIKSOKVODILAEYIGRLTETNEVT	360
QY	361	DSDFETRNFWIGLTYRTAKDSFRWANGEHQAFTSFAFGQPDNGLVLSAMGFGNCVEL	420
DB	361	DSDFETRNFWIGLTYRTAKDSFRWANGEHQAFTSFAFGQPDNGLVLSAMGFGNCVEL	420
QY	421	QASAFNMNDQRCRTNRNYICQFAQEHISRMPGS 455	
DB	412	QASAFNMNDQRCRTNRNYICQFAQEHISRMPGS 446	

Search completed: September 17, 2003, 14:00:33
Job time : 0.001 secs

